

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,567
Source: P4/10
Date Processed by STIC: 1/26/06

ENTERED



E7

RAW SEQUENCE LISTING

DATE: 01/26/2006

PATENT APPLICATION: US/10/525,567

TIME: 09:28:41

Input Set : A:\WO961SEQLIST.txt

Output Set: N:\CRF4\01262006\J525567.raw

3 <110> APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
 4 OKAMOTO, Iwao
 5 ARAI, Norie
 6 KOHNO, Keizo
 7 KURIMOTO, Masashi
 8 SANO, Osamu
 10 <120> TITLE OF INVENTION: ANTI-ALLERGIC AGENT
 12 <130> FILE REFERENCE: OKAMOTO11
 14 <140> CURRENT APPLICATION NUMBER: 10/525,567
 15 <141> CURRENT FILING DATE: 2005-02-25
 17 <150> PRIOR APPLICATION NUMBER: JP 2002-252087
 18 <151> PRIOR FILING DATE: 2002-08-29
 20 <150> PRIOR APPLICATION NUMBER: JP 2003-22776
 21 <151> PRIOR FILING DATE: 2003-01-30
 23 <160> NUMBER OF SEQ ID NOS: 12
 25 <170> SOFTWARE: PatentIn version 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 10
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Apis mellifera
 32 <400> SEQUENCE: 1
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 35 1 5 10
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 25
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Apis mellifera
 43 <400> SEQUENCE: 2
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 46 1 5 10 15
 49 Glu Trp Lys Phe Phe Asp Tyr Asp Phe
 50 20 25
 53 <210> SEQ ID NO: 3
 54 <211> LENGTH: 524
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Apis mellifera
 58 <400> SEQUENCE: 3
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 61 1 5 10 15
 64 Met Lys Val Ile Tyr Glu Trp Lys His Ile Asp Phe Asp Phe Gly Ser
 65 20 25 30
 68 Asp Glu Arg Arg Asp Ala Ala Ile Lys Ser Gly Glu Phe Asp His Thr
 69 35 40 45

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72 Lys Asn Tyr Pro Phe Asp Val Asp Arg Trp Arg Asp Lys Thr Phe Val
73      50                      55                      60
76 Thr Ile Glu Arg Asn Asn Gly Val Pro Ser Ser Leu Asn Val Val Thr
77 65                      70                      75                      80
80 Asn Lys Lys Gly Lys Gly Gly Pro Leu Leu Arg Pro Tyr Pro Asp Trp
81                      85                      90                      95
84 Ser Phe Ala Lys Tyr Glu Asp Cys Ser Gly Ile Val Ser Ala Phe Lys
85      100                      105                      110
88 Ile Ala Val Asp Lys Phe Asp Arg Leu Trp Val Leu Asp Ser Gly Leu
89      115                      120                      125
92 Val Asn Asn Asn Gln Pro Met Cys Ser Pro Lys Leu Leu Thr Phe Asp
93      130                      135                      140
96 Leu Lys Thr Ser Lys Leu Val Lys Gln Val Glu Ile Pro His Asn Ile
97 145                      150                      155                      160
100 Ala Val Asn Ala Thr Thr Gly Met Gly Glu Leu Val Ser Leu Ala Val
101                      165                      170                      175
104 Gln Ala Ile Asp Arg Thr Asn Thr Met Val Tyr Ile Ala Asp Glu Lys
105      180                      185                      190
108 Gly Glu Gly Leu Ile Met Tyr Gln Asn Ser Asp Asp Ser Phe His Arg
109      195                      200                      205
112 Leu Thr Ser Asn Thr Phe Asp Tyr Asp Pro Arg Tyr Thr Lys Leu Thr
113      210                      215                      220
116 Val Ala Gly Glu Ser Phe Thr Val Lys Asn Gly Ile Cys Gly Ile Ala
117 225                      230                      235                      240
120 Leu Ser Pro Val Thr Asn Asn Leu Tyr Tyr Ser Pro Leu Ser Ser His
121      245                      250                      255
124 Gly Leu Tyr Tyr Val Asp Thr Glu Gln Phe Arg Asn Pro Gln Tyr Glu
125      260                      265                      270
128 Glu Asn Asn Val Gln Tyr Glu Gly Ser Gln Asp Ile Leu Asn Thr Gln
129      275                      280                      285
132 Ser Phe Gly Lys Val Val Ser Lys Asn Gly Val Leu Phe Leu Gly Leu
133      290                      295                      300
136 Val Gly Asn Ser Gly Ile Ala Cys Val Asn Glu His Gln Val Leu Gln
137 305                      310                      315                      320
140 Arg Glu Ser Phe Asp Val Val Ala Gln Asn Glu Glu Thr Leu Gln Met
141      325                      330                      335
144 Ile Val Ser Met Lys Ile Met Glu Asn Leu Pro Gln Ser Gly Arg Ile
145      340                      345                      350
148 Asn Asp Pro Glu Gly Asn Glu Tyr Met Leu Ala Leu Ser Asn Arg Met
149      355                      360                      365
152 Gln Lys Ile Ile Asn Asn Asp Phe Asn Phe Asn Asp Val Asn Phe Arg
153      370                      375                      380
156 Ile Leu Gly Ala Asn Val Asp Asp Leu Met Arg Asn Thr Arg Cys Gly
157 385                      390                      395                      400
160 Arg Tyr His Asn Gln Asn Ala Gly Asn Gln Asn Ala Asp Asn Gln Asn
161      405                      410                      415
164 Ala Asp Asn Gln Asn Ala Asn Asn Gln Asn Ala Asp Asn Gln Asn Ala
165      420                      425                      430
168 Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Arg Gln Asn Asp Asn

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169          435          440          445
172 Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg
173          450          455          460
176 Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Gly Asn Lys Gln
177 465          470          475          480
180 Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Lys Arg Asn
181          485          490          495
184 Gly Asn Arg Gln Asn Asp Asn Gln Asn Asn Gln Asn Asp Asn Asn Arg
185          500          505          510
188 Asn Asp Asn Gln Val His His Ser Ser Lys Leu His
189          515          520
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193 <211> LENGTH: 413
194 <212> TYPE: PRT
195 <213> ORGANISM: Apis mellifera
198 <220> FEATURE:
199 <221> NAME/KEY: misc_feature
200 <222> LOCATION: (344)..(344)
201 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
203 <400> SEQUENCE: 4
205 Asn Ile Leu Arg Gly Glu Ser Leu Asn Lys Ser Leu Pro Ile Leu His
206 1          5          10          15
209 Glu Trp Lys Phe Phe Asp Tyr Asp Phe Gly Ser Asp Glu Arg Arg Gln
210          20          25          30
213 Asp Ala Ile Leu Ser Gly Glu Tyr Asp Tyr Lys Asn Asn Tyr Pro Ser
214          35          40          45
217 Asp Ile Asp Gln Trp His Asp Lys Ile Phe Val Thr Met Leu Arg Tyr
218          50          55          60
221 Asn Gly Val Pro Ser Ser Leu Asn Val Ile Ser Lys Lys Val Gly Asp
222 65          70          75          80
225 Gly Gly Pro Leu Leu Gln Pro Tyr Pro Asp Trp Ser Phe Ala Lys Tyr
226          85          90          95
229 Asp Asp Cys Ser Gly Ile Val Ser Ala Ser Lys Leu Ala Ile Asp Lys
230          100          105          110
233 Cys Asp Arg Leu Trp Val Leu Asp Ser Gly Leu Val Asn Asn Thr Gln
234          115          120          125
237 Pro Met Cys Ser Pro Lys Leu Leu Thr Phe Asp Leu Thr Thr Ser Gln
238          130          135          140
241 Leu Leu Lys Gln Val Glu Ile Pro His Asp Val Ala Val Asn Ala Thr
242 145          150          155          160
245 Thr Gly Lys Gly Arg Leu Ser Ser Leu Ala Val Gln Ser Leu Asp Cys
246          165          170          175
249 Asn Thr Asn Ser Asp Thr Met Val Tyr Ile Ala Asp Glu Lys Gly Glu
250          180          185          190
253 Gly Leu Ile Val Tyr His Asn Ser Asp Asp Ser Phe His Arg Leu Thr
254          195          200          205
257 Ser Asn Thr Phe Asp Tyr Asp Pro Lys Phe Thr Lys Met Thr Ile Asp
258          210          215          220
261 Gly Glu Ser Tyr Thr Ala Gln Asp Gly Ile Ser Gly Met Ala Leu Ser

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262 225                230                235                240
265 Pro Met Thr Asn Asn Leu Tyr Tyr Ser Pro Val Ala Ser Thr Ser Leu
266                245                250                255
269 Tyr Tyr Val Asn Thr Glu Gln Phe Arg Thr Ser Asp Tyr Gln Gln Asn
270                260                265                270
273 Asp Ile His Tyr Glu Gly Val Gln Asn Ile Leu Asp Thr Gln Ser Ser
274                275                280                285
277 Ala Lys Val Val Ser Lys Ser Gly Val Leu Phe Phe Gly Leu Val Gly
278                290                295                300
281 Asp Ser Ala Leu Gly Cys Trp Asn Glu His Arg Thr Leu Glu Arg His
282 305                310                315                320
285 Asn Ile Arg Thr Val Ala Gln Ser Asp Glu Thr Leu Gln Met Ile Ala
286                325                330                335
-> 289 Ser Met Lys Ile Lys Glu Ala Xaa Pro His Val Pro Ile Phe Asp Arg
290                340                345                350
293 Tyr Ile Asn Arg Glu Tyr Ile Leu Val Leu Ser Asn Lys Met Gln Lys
294                355                360                365
297 Met Val Asn Asn Asp Phe Asn Phe Asp Asp Val Asn Phe Arg Ile Met
298                370                375                380
301 Asn Ala Asn Val Asn Glu Leu Ile Leu Asn Thr Arg Cys Glu Asn Pro
302 385                390                395                400
305 Asp Asn Asp Arg Thr Pro Phe Lys Ile Ser Ile His Leu
306                405                410
309 <210> SEQ ID NO: 5
310 <211> LENGTH: 1635
311 <212> TYPE: DNA
312 <213> ORGANISM: Apis mellifera
315 <220> FEATURE:
316 <221> NAME/KEY: CDS
317 <222> LOCATION: (1)..(1632)
319 <220> FEATURE:
320 <221> NAME/KEY: mat_peptide
321 <222> LOCATION: (61)..(1635)
323 <400> SEQUENCE: 5
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325 Met Thr Lys Trp Leu Leu Leu Val Val Cys Leu Gly Ile Ala Cys Gln
326 -20                -15                -10                -5
328 gat gta aca agc gca gct gtg aat cat caa aga aaa tct gca aat aat      96
329 Asp Val Thr Ser Ala Ala Val Asn His Gln Arg Lys Ser Ala Asn Asn
330                -1 1                5                10
332 ttg gca cat tct atg aaa gtg atc tac gaa tgg aaa cac att gat ttt      144
333 Leu Ala His Ser Met Lys Val Ile Tyr Glu Trp Lys His Ile Asp Phe
334                15                20                25
336 gat ttc ggt agc gat gaa aga aga gat gct gcg att aaa tct ggc gaa      192
337 Asp Phe Gly Ser Asp Glu Arg Arg Asp Ala Ala Ile Lys Ser Gly Glu
338                30                35                40
340 ttt gat cac aca aaa aat tat cct ttc gat gtg gac aga tgg cgt gat      240
341 Phe Asp His Thr Lys Asn Tyr Pro Phe Asp Val Asp Arg Trp Arg Asp
342 45                50                55                60

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344	aag	aca	ttt	gtc	acc	ata	gaa	agg	aac	aat	ggg	gta	cct	tct	tct	ttg	288
345	Lys	Thr	Phe	Val	Thr	Ile	Glu	Arg	Asn	Asn	Gly	Val	Pro	Ser	Ser	Leu	
346				65					70					75			
348	aac	gtg	gta	act	aat	aaa	aag	ggc	aaa	ggg	gga	cct	ctt	cta	cga	cca	336
349	Asn	Val	Val	Thr	Asn	Lys	Lys	Gly	Lys	Gly	Gly	Pro	Leu	Leu	Arg	Pro	
350				80					85					90			
352	tat	cct	gat	tgg	tcg	ttt	gcc	aaa	tac	gaa	gat	tgc	tct	gga	att	gtg	384
353	Tyr	Pro	Asp	Trp	Ser	Phe	Ala	Lys	Tyr	Glu	Asp	Cys	Ser	Gly	Ile	Val	
354				95					100					105			
356	agc	gct	ttc	aaa	att	gcg	gtc	gac	aaa	ttt	gac	aga	tta	tgg	gtt	ctg	432
357	Ser	Ala	Phe	Lys	Ile	Ala	Val	Asp	Lys	Phe	Asp	Arg	Leu	Trp	Val	Leu	
358				110					115					120			
360	gac	tca	ggg	ctt	gtc	aat	aat	caa	cct	atg	tgc	tct	cca	aaa	ttg		480
361	Asp	Ser	Gly	Leu	Val	Asn	Asn	Gln	Pro	Met	Cys	Ser	Pro	Lys	Leu		
362	125					130					135				140		
364	tta	acc	ttt	gat	ctg	aaa	acc	tca	aaa	ttg	gtt	aag	caa	gtc	gag	ata	528
365	Leu	Thr	Phe	Asp	Leu	Lys	Thr	Ser	Lys	Leu	Val	Lys	Gln	Val	Glu	Ile	
366				145						150				155			
368	cca	cat	aat	att	gcc	gta	aac	gcc	acc	aca	gga	atg	gga	gaa	tta	gtt	576
369	Pro	His	Asn	Ile	Ala	Val	Asn	Ala	Thr	Thr	Gly	Met	Gly	Glu	Leu	Val	
370				160						165				170			
372	tca	cta	gct	gtt	caa	gct	ata	gat	cgt	acg	aat	act	atg	gtg	tac	ata	624
373	Ser	Leu	Ala	Val	Gln	Ala	Ile	Asp	Arg	Thr	Asn	Thr	Met	Val	Tyr	Ile	
374				175						180				185			
376	gca	gac	gaa	aaa	ggc	gaa	ggg	tta	atc	atg	tat	caa	aac	tcc	gac	gat	672
377	Ala	Asp	Glu	Lys	Gly	Glu	Gly	Leu	Ile	Met	Tyr	Gln	Asn	Ser	Asp	Asp	
378				190						195				200			
380	tcc	ttc	cat	cga	ttg	act	tcc	aat	act	ttc	gat	tac	gat	ccc	aga	tat	720
381	Ser	Phe	His	Arg	Leu	Thr	Ser	Asn	Thr	Phe	Asp	Tyr	Asp	Pro	Arg	Tyr	
382	205					210						215			220		
384	acc	aaa	ttg	aca	gtc	gct	gga	gaa	agt	ttc	aca	gtg	aaa	aat	gga	att	768
385	Thr	Lys	Leu	Thr	Val	Ala	Gly	Glu	Ser	Phe	Thr	Val	Lys	Asn	Gly	Ile	
386				225							230			235			
388	tgt	gga	att	gca	ctt	agt	ccc	gtg	acg	aac	aat	ctt	tat	tac	agc	cct	816
389	Cys	Gly	Ile	Ala	Leu	Ser	Pro	Val	Thr	Asn	Asn	Leu	Tyr	Tyr	Ser	Pro	
390				240						245				250			
392	ctc	tct	tct	cac	ggg	ttg	tat	tat	gtt	gat	acg	gaa	caa	ttc	agg	aat	864
393	Leu	Ser	Ser	His	Gly	Leu	Tyr	Tyr	Val	Asp	Thr	Glu	Gln	Phe	Arg	Asn	
394				255						260				265			
396	cca	caa	tat	gaa	gaa	aat	aac	gtg	caa	tat	gaa	gga	tct	caa	gat	att	912
397	Pro	Gln	Tyr	Glu	Glu	Asn	Asn	Val	Gln	Tyr	Glu	Gly	Ser	Gln	Asp	Ile	
398				270						275				280			
400	ttg	aac	act	caa	tca	ttc	ggg	aaa	gta	gta	tcg	aaa	aat	ggc	gtc	ctt	960
401	Leu	Asn	Thr	Gln	Ser	Phe	Gly	Lys	Val	Val	Ser	Lys	Asn	Gly	Val	Leu	
402	285					290						295			300		
404	ttc	ttg	gga	ctc	gtg	ggg	aat	tca	ggg	att	gcc	tgc	gtg	aat	gaa	cat	1008
405	Phe	Leu	Gly	Leu	Val	Gly	Asn	Ser	Gly	Ile	Ala	Cys	Val	Asn	Glu	His	
406				305						310				315			
408	caa	gta	ctt	cag	aga	gaa	agt	ttt	gat	gtt	gtc	gct	cag	aat	gaa	gag	1056

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/525,567

DATE: 01/26/2006
TIME: 09:28:42

Input Set : A:\WO961SEQLIST.txt
Output Set: N:\CRF4\01262006\J525567.raw

Base Note:

One or more of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 344

Seq#:8; N Pos. 1134

Seq#:8; Xaa Pos. 344

Invalid <213> Response:

One or more of "Artificial" only as "<213> Organism" response is incomplete, in violation of 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12

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Output Set: N:\CRF4\01262006\J525567.raw

289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:336
365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:1113
366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:1161